



#5

SEQUENCE LISTING

<110> Prayaga, Sudhirdas
Shimkets, Richard

<120> NOVEL INTERFERON OMEGA AND NUCLEIC ACIDS ENCODING SAME

<130> 15966-615

<140> 09/732,436

<141> 2000-12-07

<150> 60/169,887

<151> 1999-12-09

<150> 60/170,230

<151> 1999-12-10

<160> 22

<170> PatentIn Ver. 2.0

<210> 1

<211> 475

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Curagen clone
AC015663_A

<400> 1

Ala Cys Cys Ala Ala Thr Gly Gly Thr Cys Thr Cys Cys Thr Thr Gly
1 5 10 15

Cys Thr Gly Gly Thr Gly Gly Cys Ala Thr Thr Gly Gly Thr Gly Ala
20 25 30

Thr Gly Ala Thr Cys Thr Cys Cys Thr Gly Cys Cys Ala Cys Ala Thr
35 40 45

Cys Thr Ala Thr Thr Cys Cys Cys Thr Thr Thr Thr Cys Thr Gly Cys
50 55 60

Gly Ala Cys Cys Thr Gly Cys Cys Thr Ala Ala Ala Gly Cys Thr Cys
65 70 75 80

Ala Gly Gly Thr Gly Ala Thr Thr Thr Cys Thr Gly Cys Cys Cys Thr

	85		90		95
Cys Cys Ala Thr Ala Ala Gly Ala Thr Gly Cys Ala Cys Cys Ala Gly	100		105		110
Cys Ala Gly Ala Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr	115		120		125
Thr Thr Thr Thr Ala Cys Ala Cys Ala Ala Gly Gly Gly Cys Thr Thr	130		135		140
Gly Thr Cys Thr Gly Ala Thr Gly Cys Thr Thr Gly Gly Ala Ala Thr	145		150		155
					160
Ala Gly Gly Gly Cys Cys Thr Thr Cys Cys Thr Gly Gly Ala Cys Ala	165		170		175
Ala Ala Cys Thr Cys Cys Ala Gly Ala Cys Thr Gly Gly Ala Thr Thr	180		185		190
Thr Cys Ala Thr Cys Ala Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala	195		200		205
Gly Ala Cys Cys Thr Gly Gly Ala Gly Ala Cys Cys Thr Gly Cys Thr	210		215		220
Thr Thr Gly Gly Thr Ala Thr Ala Gly Ala Gly Gly Ala Thr Gly Gly	225		230		235
					240
Gly Ala Ala Gly Cys Ala Ala Gly Ala Gly Thr Cys Thr Gly Cys Cys	245		250		255
Cys Thr Gly Gly Ala Ala Ala Thr Thr Gly Ala Gly Gly Gly Cys Cys	260		265		270
Cys Thr Ala Cys Ala Cys Thr Gly Gly Cys Cys Ala Thr Ala Ala Ala	275		280		285
Gly Ala Gly Gly Thr Ala Cys Thr Thr Cys Cys Ala Gly Gly Gly Ala	290		295		300
Gly Thr Ala Cys Ala Thr Thr Thr Cys Thr Thr Cys Thr Thr Gly Ala	305		310		315
					320
Ala Ala Gly Ala Gly Ala Gly Gly Ala Ala Ala Thr Thr Cys Ala Gly	325		330		335
Gly Ala Ala Cys Thr Gly Thr Ala Cys Cys Thr Gly Gly Gly Ala Gly					

Gly Ala Cys Cys Thr Gly Cys Cys Thr Asn Asn Asn Asn Asn Asn Asn
 65 70 75 80
 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
 85 90 95
 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
 100 105 110
 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
 115 120 125
 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
 130 135 140
 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
 145 150 155 160
 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
 165 170 175
 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
 180 185 190
 Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
 195 200 205
 Ala Ala Ala Gly Cys Thr Cys Ala Gly Gly Thr Gly Ala Thr Thr Thr
 210 215 220
 Cys Thr Gly Cys Cys Cys Thr Cys Cys Ala Thr Ala Ala Gly Ala Thr
 225 230 235 240
 Gly Cys Ala Cys Cys Ala Gly Cys Ala Gly Ala Thr Cys Thr Thr Cys
 245 250 255
 Ala Gly Cys Cys Thr Cys Thr Thr Thr Thr Thr Ala Cys Ala Cys Ala
 260 265 270
 Ala Gly Gly Gly Cys Thr Thr Gly Thr Cys Thr Gly Ala Thr Gly Cys
 275 280 285
 Thr Thr Gly Gly Ala Ala Thr Ala Gly Gly Gly Cys Cys Thr Thr Cys
 290 295 300
 Cys Thr Gly Gly Ala Cys Ala Ala Ala Cys Thr Cys Cys Ala Gly Ala
 305 310 315 320

Cys Thr Gly Gly Ala Thr Thr Thr Cys Ala Thr Cys Ala Gly Cys Ala
325 330 335

Gly Cys Thr Gly Gly Ala Ala Gly Ala Cys Cys Thr Gly Gly Ala Gly
340 345 350

Ala Cys Cys Thr Gly Cys Thr Thr Thr Gly Gly Thr Ala Thr Ala Gly
355 360 365

Ala Gly Gly Ala Thr Gly Gly Gly Ala Ala Gly Cys Ala Ala Gly Ala
370 375 380

Gly Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly Ala Ala Ala Thr Thr
385 390 395 400

Gly Ala Gly Gly Gly Cys Cys Cys Thr Ala Cys Ala Cys Thr Gly Gly
405 410 415

Cys Cys Ala Thr Ala Ala Ala Gly Ala Gly Gly Thr Ala Cys Thr Thr
420 425 430

Cys Cys Ala Gly Gly Gly Ala Gly Thr Ala Cys Ala Thr Thr Thr Cys
435 440 445

Thr Thr Cys Thr Thr Gly Ala Ala Ala Gly Ala Gly Ala Gly Gly Ala
450 455 460

Ala Ala Thr Thr Cys Ala Gly Gly Ala Ala Cys Thr Gly Thr Ala Cys
465 470 475 480

Cys Thr Gly Gly Gly Ala Gly Gly Thr Thr Gly Thr Cys Gly Thr Ala
485 490 495

Ala Thr Gly Gly Thr Ala Ala Ala Gly Gly Gly Ala Thr Thr Thr Thr
500 505 510

Thr Cys Thr Thr Ala Ala Gly Cys Ala Cys Ala Ala Ala Ala Cys Thr
515 520 525

Thr Cys Ala Ala Gly Ala Ala Ala Ala Ala Gly Ala Gly Ala Ala Cys
530 535 540

Ala Gly Ala Ala Gly Ala Ala Ala Ala Gly Ala Gly Ala Ala Cys Thr
545 550 555 560

Gly Cys Ala Ala Ala Ala Ala Ala Ala Thr Cys Thr Gly Gly Ala
565 570 575

Ala Ala Ala Gly Gly Thr Ala Ala Thr Cys Thr Ala Thr Thr Thr Ala
580 585 590

Gly Cys Ala Gly Ala Ala Gly Ala Gly Thr Gly Ala Ala Ala Gly Cys
595 600 605

Thr Gly
610

<210> 3
<211> 1887
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Curagen clone
AF038458_A

<400> 3
atggccatcc tcccgttgct cctgtgcctg ctgccgctgg cccctgcctc atccccaccc 60
cagtcagcca caccagccc atgtccccgc cgctgccgct gccagacaca gtcgctgccc 120
ctaagcgtgc tgtgcccagg ggcaggcctc ctgttcgtgc caccctcgct ggaccgcccg 180
gcagccgagc tgcggctggc agacaacttc atcgccctcg tgcgcccgcg cgacctggcc 240
aacatgacag gcctgctgca tctgagcctg tcgcggaaca ccatccgcca cgtggctgcc 300
ggcgcccttcg ccgacctgcg ggccctgcgt gccctgcacc tggatggcaa ccggctgacc 360
tactggggcg agggccagct gcgcggcctg gtcaacttgc gccacctcat cctcagcaac 420
aaccagctgg cagcgctggc ggccggcgcc ctggatgatt gtgccgagac actggaggac 480
ctcgacctct cctacaacaa cctcgagcag ctgccctggg aggccctggg ccgcctgggc 540
aacgtcaaca cgttgggcct cgaccacaac ctgctggctt ctgtgccgcg cggcgctttt 600
tccgcctgc acaagctggc ccggctggac atgacctcca accgcctgac cacaatccca 660
cccgacccac tcttctcccg cctgcccctg ctgcgccagg cccggggctc gcccgcctct 720
gccctggtgc tggccttttg cgggaacccc ctgcaactgca actgcgagct ggtgtggctg 780
cgtcgcctgg cgcgggagga cgacctcgag gcctgcgcgt cccacctgc tctgggcggc 840
cgctacttct gggcggtggg cgaggaggag tttgtctgcg agccgcccgt ggtgactcac 900
cgctcaccac ctctggtgtg gcccgaggt cgcccggtg cctgcgctg ccgggcagtg 960
ggggacccag agccccgtgt gcgttgggtg tcacccag gccggctgct aggcaactca 1020
agccgtgccc gcgccttccc caatgggacg ctggagctgc tggtcaccga gccgggtgat 1080
ggtggcatct tcacctgcat tgcggccaat gcagctggcg aggccacagc tgctgtggag 1140
ctgactgtgg gtccccacc acctcctcag ctagccaaca gcaccagctg tgaccccccg 1200
cgggacgggg atcctgatgc tctcacccca ccctccgctg cctctgcttc tgccaagggtg 1260
gccgacactg gggcccctac cgacctggc gtccagggtga ctgagcacgg ggccacagct 1320
gctcttgtcc agtggccgga tcagcggcct atcccgggca tccgcatgta ccagatccag 1380
tacaacagct cggtgatga catcctcgtc tacaggatga tcccggcgga gagccgctcg 1440
ttcctgctga cggacctggc gtcaggccgg acctacgata tgtgcgtgct cgccgtgtat 1500
gaggacagcg ccacggggct caccggccag cggcctgtgg gctgcgcccg cttctccacc 1560
gaacctgcgc tgcggccatg cggggcgccg cagctccct tctggggcg cagcatgata 1620
atcgcgctgg gcggcgctcat cgtagcctcg gtactggtct tcatcttcgt gctgctaata 1680

cgctacaagg tgcacggcgg ccagcccccc ggcaaggcca agattcccgc gcctgttagc 1740
 agcgtttgcg cccagaccaa cggcgccctg ggccccacgc ccacgcccgc cccgcccgc 1800
 ccggagcccg cggcgctcag ggcccacacc gtggtccagc tggactgcga gccctggggg 1860
 cccggccacg aacctgtggg acctag 1887

<210> 4
 <211> 365
 <212> PRT
 <213> Equus caballus

<400> 4
 Thr Cys Cys Cys Ala Gly Ala Gly Gly Cys Cys Cys Ala Gly Gly Cys
 1 5 10 15
 Cys Gly Cys Gly Thr Cys Thr Gly Thr Cys Cys Thr Cys Cys Ala Cys
 20 25 30
 Gly Ala Gly Ala Thr Gly Cys Thr Cys Cys Ala Gly Cys Ala Gly Ala
 35 40 45
 Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr Thr Cys Cys Ala
 50 55 60
 Cys Ala Cys Ala Gly Ala Gly Cys Gly Cys Thr Cys Gly Thr Cys Thr
 65 70 75 80
 Gly Cys Thr Gly Cys Cys Thr Gly Gly Ala Ala Cys Ala Cys Gly Ala
 85 90 95
 Cys Cys Cys Thr Cys Cys Thr Gly Gly Ala Cys Gly Ala Ala Cys Thr
 100 105 110
 Cys Thr Gly Cys Ala Cys Gly Gly Gly Ala Cys Thr Cys Cys Thr Thr
 115 120 125
 Cys Gly Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala Gly Ala Cys Cys
 130 135 140
 Thr Gly Gly Ala Cys Ala Cys Cys Thr Gly Thr Thr Thr Gly Gly Ala
 145 150 155 160
 Gly Cys Ala Gly Gly Ala Gly Ala Thr Gly Gly Gly Ala Gly Ala Gly
 165 170 175
 Gly Ala Ala Gly Ala Ala Thr Cys Thr Gly Cys Cys Cys Thr Gly Gly
 180 185 190
 Gly Ala Ala Cys Thr Gly Thr Gly Cys Gly Cys Cys Cys Thr Ala Cys

195	200	205
Ala Cys Thr Gly Gly Cys Cys Gly Thr Gly Ala Ala Gly Ala Gly Gly		
210	215	220
Thr Ala Cys Thr Thr Cys Cys Gly Gly Gly Gly Gly Ala Thr Cys Cys		
225	230	235 240
Ala Thr Cys Thr Cys Thr Ala Cys Cys Thr Gly Ala Ala Ala Gly Ala		
	245	250 255
Gly Ala Ala Gly Ala Ala Ala Thr Ala Cys Ala Gly Thr Gly Ala Cys		
	260	265 270
Thr Gly Thr Gly Cys Cys Thr Gly Gly Gly Ala Gly Ala Thr Thr Gly		
	275	280 285
Thr Cys Cys Gly Ala Ala Thr Gly Gly Ala Ala Ala Thr Cys Ala Thr		
	290	295 300
Gly Ala Gly Ala Thr Cys Cys Thr Thr Cys Thr Cys Thr Thr Cys Ala		
305	310	315 320
Thr Cys Ala Gly Cys Ala Ala Ala Cys Cys Thr Gly Cys Ala Ala Gly		
	325	330 335
Gly Ala Ala Gly Gly Thr Thr Ala Ala Gly Ala Ala Thr Gly Ala Ala		
	340	345 350
Gly Gly Ala Thr Gly Gly Ala Gly Ala Cys Cys Thr Gly		
	355	360 365

<210> 5
 <211> 132
 <212> PRT
 <213> Homo sapiens

<400> 5
 Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr
 1 5 10 15
 Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu
 20 25 30
 Leu Ser Arg Asn Thr Leu Val Phe Pro Gln Glu Met Val Lys Gly Ser
 35 40 45

Gln Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met Leu Gln
50 55 60

Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala Thr Cys
65 70 75 80

Leu Leu Gln Val Val Gly Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser
85 90 95

Pro Ala Leu Thr Leu Arg Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu
100 105 110

Lys Glu Lys Lys Tyr Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp
115 120 125

Leu Gly Ser Ser
130

<210> 6

<211> 132

<212> PRT

<213> Equus caballus

<400> 6

Met Ala Phe Ser Val Ser Ser Leu Met Ala Leu Val Val Ile Ser Ser
1 5 10 15

Ser Pro Val Ser Ser Met Ser Cys Asp Leu Pro Ala Ser Leu Asp Leu
20 25 30

Arg Lys Gln Glu Thr Leu Arg Phe Pro Gln Glu Gln Leu Asp Gly Arg
35 40 45

Gln Phe Pro Glu Ala Gln Ala Thr Ser Val Leu Gln Glu Met Leu Gln
50 55 60

Gln Ile Val Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala Thr Cys
65 70 75 80

Leu Asp Glu Gln Thr Gly Glu Glu Glu Ser Ala Leu Gly Thr Val Gly
85 90 95

Pro Thr Leu Ala Val Lys Arg Tyr Phe Arg Arg Ile Arg Leu Tyr Leu
100 105 110

Thr Glu Lys Lys Tyr Leu Gln Gly Arg Leu Gly Met Lys Asp Gly Asp
115 120 125

Leu Gly Ser Pro
130

<210> 7
<211> 475
<212> PRT
<213> Homo sapiens

<400> 7
Ala Cys Cys Ala Ala Thr Gly Gly Thr Cys Thr Cys Cys Thr Thr Gly
1 5 10 15
Cys Thr Gly Gly Thr Gly Gly Cys Ala Thr Thr Gly Gly Thr Gly Ala
20 25 30
Thr Gly Ala Thr Cys Thr Cys Cys Thr Gly Cys Cys Ala Cys Ala Thr
35 40 45
Cys Thr Ala Thr Thr Cys Cys Cys Thr Thr Thr Thr Cys Thr Gly Cys
50 55 60
Gly Ala Cys Cys Thr Gly Cys Cys Thr Ala Ala Ala Gly Cys Thr Cys
65 70 75 80
Ala Gly Gly Thr Gly Ala Thr Thr Thr Cys Thr Gly Cys Cys Cys Thr
85 90 95
Cys Cys Ala Thr Ala Ala Gly Ala Thr Gly Cys Ala Cys Cys Ala Gly
100 105 110
Cys Ala Gly Ala Thr Cys Thr Thr Cys Ala Gly Cys Cys Thr Cys Thr
115 120 125
Thr Thr Thr Thr Ala Cys Ala Cys Ala Ala Gly Gly Gly Cys Thr Thr
130 135 140
Gly Thr Cys Thr Gly Ala Thr Gly Cys Thr Thr Gly Gly Ala Ala Thr
145 150 155 160
Ala Gly Gly Gly Cys Cys Thr Thr Cys Cys Thr Gly Gly Ala Cys Ala
165 170 175
Ala Ala Cys Thr Cys Cys Ala Gly Ala Cys Thr Gly Gly Ala Thr Thr
180 185 190
Thr Cys Ala Thr Cys Ala Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala

195	200	205
Gly Ala Cys Cys Thr Gly Gly Ala Gly Ala Cys Cys Thr Gly Cys Thr		
210	215	220
Thr Thr Gly Gly Thr Ala Thr Ala Gly Ala Gly Gly Ala Thr Gly Gly		
225	230	235 240
Gly Ala Ala Gly Cys Ala Ala Gly Ala Gly Thr Cys Thr Gly Cys Cys		
245	250	255
Cys Thr Gly Gly Ala Ala Ala Thr Thr Gly Ala Gly Gly Gly Cys Cys		
260	265	270
Cys Thr Ala Cys Ala Cys Thr Gly Gly Cys Cys Ala Thr Ala Ala Ala		
275	280	285
Gly Ala Gly Gly Thr Ala Cys Thr Thr Cys Cys Ala Gly Gly Gly Ala		
290	295	300
Gly Thr Ala Cys Ala Thr Thr Thr Cys Thr Thr Cys Thr Thr Gly Ala		
305	310	315 320
Ala Ala Gly Ala Gly Ala Gly Gly Ala Ala Ala Thr Thr Cys Ala Gly		
325	330	335
Gly Ala Ala Cys Thr Gly Thr Ala Cys Cys Thr Gly Gly Gly Ala Gly		
340	345	350
Gly Thr Thr Gly Thr Cys Gly Thr Ala Ala Thr Gly Gly Thr Ala Ala		
355	360	365
Ala Gly Gly Gly Ala Thr Thr Thr Thr Thr Cys Thr Thr Ala Ala Gly		
370	375	380
Cys Ala Cys Ala Ala Ala Ala Cys Thr Thr Cys Ala Ala Gly Ala Ala		
385	390	395 400
Ala Ala Ala Gly Ala Gly Ala Ala Cys Ala Gly Ala Ala Gly Ala Ala		
405	410	415
Ala Ala Gly Ala Gly Ala Ala Cys Thr Gly Cys Ala Ala Ala Ala Ala		
420	425	430
Ala Ala Ala Thr Cys Thr Gly Gly Ala Ala Ala Ala Gly Gly Thr Ala		
435	440	445
Ala Thr Cys Thr Ala Thr Thr Thr Ala Gly Cys Ala Gly Ala Ala Gly		

450

455

460

Ala Gly Thr Gly Ala Ala Ala Gly Cys Thr Gly
 465 470 475

<210> 8
 <211> 70
 <212> DNA
 <213> Unknown

<220>

<223> Description of Unknown Organism: Interferon Alpha
 Precursor

<400> 8
 shkaasvvhv tnkhctasss aawnttctgd rtracvvgat ndhdsrnyrs ykkyscawvr 60
 amrsyyssta 70

<210> 9
 <211> 112
 <212> PRT
 <213> Unknown

<220>

<223> Description of Unknown Organism: Interferon
 Delta-1 Precursor

<400> 9
 Leu Gln Glu Ala Gln Ala Ile Ser Val Leu His Glu Met Leu Gln Gln
 1 5 10 15
 Ser Phe Asn Leu Phe His Thr Glu His Ser Ser Ala Ala Trp Asp Thr
 20 25 30
 Thr Leu Leu Glu Pro Cys Arg Thr Gly Leu His Gln Gln Leu Asp Asn
 35 40 45
 Leu Asp Ala Cys Leu Gly Gln Val Met Gly Glu Glu Asp Ser Ala Leu
 50 55 60
 Gly Arg Thr Gly Pro Thr Leu Ala Leu Lys Arg Tyr Phe Gln Gly Ile
 65 70 75 80
 His Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp Cys Ala Trp Glu Thr
 85 90 95
 Val Arg Leu Glu Ile Met Arg Ser Phe Ser Ser Leu Ile Ser Leu Gln

100

105

110

<210> 10

<211> 112

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Interferon
 Omega-2 Precursor (Interferon Alpha-II-2)

<400> 10

Phe Pro Glu Ala Gln Ala Ala Ser Val Leu His Glu Met Leu Gln Gln
 1 5 10 15

Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala Trp Asn Thr
 20 25 30

Thr Leu Leu Asp Glu Leu Cys Thr Gly Leu Leu Arg Gln Leu Glu Asp
 35 40 45

Leu Asp Thr Cys Leu Glu Gln Glu Met Gly Glu Glu Glu Ser Ala Leu
 50 55 60

Gly Thr Val Arg Pro Thr Leu Ala Val Lys Arg Tyr Phe Arg Gly Ile
 65 70 75 80

His Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp Glu Ile
 85 90 95

Val Arg Met Glu Ile Met Arg Ser Phe Ser Ser Ser Ala Asn Leu Gln
 100 105 110

<210> 11

<211> 112

<212> PRT

<213> Unknown

<400> 11

Leu Gln Lys Ala His Val Met Ser Val Leu His Glu Met Leu Gln Gln

1	5	10	15
Ile Phe Ser Leu Phe His Thr Glu Arg Ser Ser Ala Ala Trp Asn Met			
20	25	30	
Thr Leu Leu Asp Gln Leu His Thr Gly Leu His Gln Gln Leu Gln His			
35	40	45	
Leu Glu Thr Cys Leu Leu Gln Val Val Gly Glu Gly Glu Ser Ala Gly			
50	55	60	
Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe Gln Gly Ile			
65	70	75	80
Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp Glu Val			
85	90	95	
Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr Asn Met Gln			
100	105	110	

<210> 12

<211> 65

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Interferon

<400> 12

Ala Gln Ser Val Leu His Met Gln Gln Ile Phe Leu Phe Thr Glu Ser			
1	5	10	15
Ser Ala Ala Trp Asn Thr Leu Leu Thr Gly Leu Gln Leu Leu Cys Gln			
20	25	30	
Gly Glu Glu Ser Ala Leu Pro Leu Arg Tyr Phe Gln Gly Tyr Leu Lys			
35	40	45	
Glu Lys Lys Tyr Ser Cys Ala Trp Glu Val Arg Glu Ile Met Ser Leu			
50	55	60	
Gln			
65			

<210> 13
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 13
 Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys
 1 5 10 15
 Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala
 20 25 30
 Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val
 35 40 45
 Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr
 50 55 60
 Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu
 65 70 75 80
 Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr
 85 90 95
 Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val
 100 105 110

<210> 14
 <211> 109
 <212> PRT
 <213> Homo sapiens

<400> 14
 Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala
 1 5 10 15
 Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu
 20 25 30
 Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp
 35 40 45
 Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys
 50 55 60
 Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Asn Glu Asp

65 70 75 80
 Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu Tyr Leu
 85 90 95

Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 100 105

<210> 15
 <211> 110
 <212> PRT
 <213> Unknown

<220>
 <223> Description of Unknown Organism: Interferon
 Alpha-1 Precursor

<400> 15
 Asp Phe Gly Phe Pro Gln Glu Lys Val Asp Ala Gln Gln Ile Lys Lys
 1 5 10 15

Ala Gln Ala Ile Pro Val Leu Ser Glu Leu Thr Gln Gln Ile Leu Asn
 20 25 30

Ile Phe Thr Ser Lys Asp Ser Ser Ala Ala Trp Asn Ala Thr Leu Leu
 35 40 45

Asp Ser Phe Cys Asn Asp Leu His Gln Gln Leu Asn Asp Leu Gln Gly
 50 55 60

Cys Leu Met Gln Gln Val Gly Val Gln Glu Phe Pro Leu Thr Gln Glu
 65 70 75 80

Asp Ala Leu Leu Ala Val Arg Lys Tyr Phe His Arg Ile Thr Val Tyr
 85 90 95

Leu Arg Glu Lys Lys His Ser Pro Cys Ala Trp Glu Val Val
 100 105 110

<210> 16
 <211> 110
 <212> PRT
 <213> Rabbitt Interferon-omega20

<400> 16
 Asp Phe Gln Phe Pro Arg Glu Val Val Asn Gly Ser Gln Phe Gln Lys

1	5	10	15
Asn Gln Thr Val Ser Val Leu His Glu Met Leu Gln Gln Ile Phe Asn			
20	25	30	
Leu Leu His Thr Ala Arg Ser Ser Ala Ala Trp Asn Asn Thr Leu Leu			
35	40	45	
Glu Glu Leu His Thr Ala Leu His Gln Gln Leu Gln Gly Leu Glu Thr			
50	55	60	
Cys Leu Val Gln Ala Met Gly Glu Glu Asp Ser Val Leu Thr Ala Asp			
65	70	75	80
Ser Pro Met Leu Met Leu Lys Arg Tyr Phe Gln Arg Ile Arg Leu Tyr			
85	90	95	
Leu Asp Glu Lys Lys His Ser Gly Cys Ala Trp Glu Leu Val			
100	105	110	

<210> 17

<211> 43

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus of
SEQ ID NO:1 and SEQ ID NOS:16-19

<400> 17

Phe Pro Glu Gln Lys Leu Glu Met Gln Gln Ile Phe Phe Ser Ser Ala
1 5 10 15

Trp Asn Thr Leu Gln Gln Leu Leu Cys Gly Leu Leu Tyr Phe Arg Ile
20 25 30

Tyr Leu Glu Lys Lys Ser Cys Ala Trp Glu Val
35 40

<210> 18

<211> 184

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Interferon

Alpha-1 Precursor

<400> 18

Val	Ser	Leu	Leu	Met	Ala	Leu	Val	Val	Leu	Ser	Cys	His	Ser	Ile	Cys
1				5					10					15	

Ser	Leu	Gly	Cys	Asp	Leu	Pro	His	Thr	His	Ser	Leu	Gly	Asn	Thr	Arg
			20					25					30		

Val	Leu	Met	Leu	Leu	Gly	Gln	Met	Arg	Arg	Ile	Ser	Pro	Phe	Ser	Cys
		35					40					45			

Leu	Lys	Asp	Arg	Asn	Asp	Phe	Gly	Phe	Pro	Gln	Glu	Val	Phe	Asp	Gly
	50					55					60				

Asn	Gln	Phe	Arg	Lys	Pro	Gln	Ala	Ile	Ser	Ala	Val	His	Glu	Thr	Ile
65					70				75						80

Gln	Gln	Ile	Phe	His	Leu	Phe	Ser	Thr	Asp	Gly	Ser	Ser	Ala	Ala	Trp
			85						90					95	

Asp	Glu	Ser	Leu	Leu	Asp	Lys	Leu	Tyr	Thr	Gly	Leu	Tyr	Gln	Gln	Leu
			100					105					110		

Thr	Glu	Leu	Glu	Ala	Cys	Leu	Ser	Gln	Glu	Val	Gly	Val	Glu	Glu	Thr
		115					120					125			

Pro	Leu	Met	Asn	Glu	Asp	Ser	Leu	Leu	Ala	Val	Arg	Arg	Tyr	Phe	Gln
	130					135					140				

Arg	Ile	Ala	Leu	Tyr	Leu	Gln	Glu	Lys	Lys	Tyr	Ser	Pro	Cys	Ala	Trp
145					150					155				160	

Glu	Ile	Val	Arg	Ala	Glu	Ile	Met	Arg	Ser	Phe	Ser	Ser	Ser	Thr	Asn
			165					170						175	

Leu	Pro	Ser	Glu	Gln	Ile	Asp	Asn
			180				

<210> 19

<211> 92

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus of
SEQ ID NO:4 and SEQ ID NOS:11, 13, 14, 21 and 22

<400> 19

Ser Leu Leu Ala Leu Val Ser Leu Gly Cys Asp Leu Pro His Leu Leu
1 5 10 15

Leu Gln Met Arg Cys Lys Asp Arg Asp Phe Phe Pro Gln Gly Gln Lys
20 25 30

Ala Gln Ser His Gln Gln Ile Phe Leu Phe Thr Ser Ser Ala Ala Trp
35 40 45

Asn Leu Leu Asp Leu Thr Gly Leu Gln Leu Leu Glu Cys Gln Glu Gly
50 55 60

Glu Leu Leu Arg Tyr Phe Gln Tyr Leu Glu Lys Lys Tyr Ser Cys Ala
65 70 75 80

Trp Glu Val Arg Glu Ile Met Ser Ser Thr Leu Gln
85 90

<210> 20

<211> 1752

<212> PRT

<213> Homo sapiens

<400> 20

Cys Gly Cys Cys Thr Gly Cys Cys Cys Cys Ala Ala Gly Thr Ala Cys
1 5 10 15

Thr Gly Thr Gly Thr Cys Thr Gly Cys Cys Ala Gly Ala Ala Thr Cys
20 25 30

Thr Gly Thr Cys Thr Gly Ala Gly Thr Cys Ala Cys Thr Gly Gly Gly
35 40 45

Gly Ala Cys Cys Cys Thr Gly Thr Gly Cys Cys Cys Cys Thr Cys Cys
50 55 60

Ala Ala Gly Gly Gly Gly Cys Thr Gly Cys Thr Cys Thr Thr Thr Gly
65 70 75 80

Thr Ala Cys Cys Cys Cys Cys Thr Gly Ala Thr Ala Thr Thr Gly Ala
85 90 95

Cys Cys Gly Gly Cys Gly Gly Ala Cys Ala Gly Thr Gly Gly Ala Gly
100 105 110

Cys Thr Gly Cys Gly Cys Cys Thr Gly Gly Gly Cys Gly Gly Cys Ala
 115 120 125

Ala Cys Thr Thr Cys Ala Thr Cys Ala Thr Cys Cys Ala Cys Ala Thr
 130 135 140

Cys Ala Gly Cys Cys Gly Cys Cys Ala Gly Gly Ala Cys Thr Thr Thr
 145 150 155 160

Gly Cys Cys Ala Ala Cys Ala Thr Gly Ala Cys Gly Gly Gly Gly Cys
 165 170 175

Thr Gly Gly Thr Gly Gly Ala Cys Cys Thr Gly Ala Cys Cys Cys Thr
 180 185 190

Gly Thr Cys Cys Ala Gly Gly Ala Ala Cys Ala Cys Cys Ala Thr Cys
 195 200 205

Ala Gly Cys Cys Ala Cys Ala Thr Cys Cys Ala Gly Cys Cys Cys Thr
 210 215 220

Thr Thr Thr Cys Cys Thr Thr Thr Cys Thr Gly Gly Ala Cys Cys Thr
 225 230 235 240

Cys Gly Ala Gly Ala Gly Cys Cys Thr Cys Cys Gly Cys Thr Cys Cys
 245 250 255

Cys Thr Gly Cys Ala Thr Cys Thr Thr Gly Ala Cys Ala Gly Cys Ala
 260 265 270

Ala Thr Cys Gly Gly Cys Thr Gly Cys Cys Ala Ala Gly Cys Cys Thr
 275 280 285

Thr Gly Gly Gly Gly Ala Gly Gly Ala Cys Ala Cys Cys Cys Thr Cys
 290 295 300

Cys Gly Gly Gly Gly Cys Cys Thr Gly Gly Thr Cys Ala Ala Cys Cys
 305 310 315 320

Thr Gly Cys Ala Gly Cys Ala Cys Cys Thr Thr Ala Thr Cys Gly Thr
 325 330 335

Gly Ala Ala Cys Ala Ala Cys Ala Ala Cys Cys Ala Gly Cys Thr Gly
 340 345 350

Gly Gly Cys Gly Gly Cys Ala Thr Cys Gly Cys Ala Gly Ala Thr Gly
 355 360 365

Ala Gly Gly Cys Thr Thr Thr Thr Gly Ala Gly Gly Ala Cys Thr Thr
 370 375 380

Cys Cys Thr Gly Cys Thr Gly Ala Cys Ala Thr Thr Gly Gly Ala Gly
 385 390 395 400

Gly Ala Thr Cys Thr Gly Gly Ala Cys Cys Thr Cys Thr Cys Cys Thr
 405 410 415

Ala Cys Ala Ala Cys Ala Ala Cys Cys Thr Cys Cys Ala Thr Gly Gly
 420 425 430

Cys Cys Thr Gly Cys Cys Gly Thr Gly Gly Gly Ala Cys Thr Cys Cys
 435 440 445

Gly Thr Gly Cys Gly Ala Cys Gly Cys Ala Thr Gly Gly Thr Cys Ala
 450 455 460

Ala Cys Cys Thr Cys Cys Ala Cys Cys Ala Gly Cys Thr Gly Ala Gly
 465 470 475 480

Cys Cys Thr Gly Gly Ala Cys Cys Ala Cys Ala Ala Cys Cys Thr Gly
 485 490 495

Cys Thr Gly Gly Ala Thr Cys Ala Cys Ala Thr Cys Gly Cys Cys Gly
 500 505 510

Ala Gly Gly Gly Cys Ala Cys Cys Thr Thr Thr Gly Cys Ala Gly Ala
 515 520 525

Cys Cys Thr Gly Cys Ala Gly Ala Ala Ala Cys Thr Gly Gly Cys Cys
 530 535 540

Cys Gly Cys Cys Thr Gly Gly Ala Thr Cys Thr Cys Ala Cys Cys Thr
 545 550 555 560

Cys Cys Ala Ala Thr Cys Gly Gly Cys Thr Gly Cys Ala Gly Ala Ala
 565 570 575

Gly Cys Thr Gly Cys Cys Cys Cys Cys Thr Gly Ala Thr Cys Cys Cys
 580 585 590

Ala Thr Cys Thr Thr Thr Gly Cys Cys Cys Gly Cys Thr Cys Cys Cys
 595 600 605

Ala Gly Gly Cys Thr Thr Cys Gly Gly Cys Thr Thr Thr Gly Ala Cys
 610 615 620

Ala Gly Cys Cys Ala Cys Ala Cys Cys Cys Thr Thr Thr Gly Cys Cys
 625 630 635 640
 Cys Cys Ala Cys Cys Cys Thr Thr Gly Thr Cys Cys Thr Thr Thr Ala
 645 650 655
 Gly Thr Thr Thr Thr Gly Gly Gly Gly Gly Thr Ala Ala Cys Cys Cys
 660 665 670
 Ala Cys Thr Thr Cys Ala Cys Thr Gly Cys Ala Ala Thr Thr Gly Thr
 675 680 685
 Gly Ala Gly Cys Thr Thr Cys Thr Cys Thr Gly Gly Cys Thr Gly Cys
 690 695 700
 Gly Gly Ala Gly Gly Cys Thr Cys Gly Ala Gly Cys Gly Gly Gly Ala
 705 710 715 720
 Cys Gly Ala Thr Gly Ala Cys Cys Thr Gly Gly Ala Ala Ala Cys Cys
 725 730 735
 Thr Gly Thr Gly Gly Cys Thr Cys Cys Cys Cys Ala Gly Gly Gly Gly
 740 745 750
 Gly Cys Cys Thr Cys Ala Ala Gly Gly Gly Thr Cys Gly Cys Thr Ala
 755 760 765
 Cys Thr Thr Cys Thr Gly Gly Cys Ala Thr Gly Thr Gly Cys Gly Thr
 770 775 780
 Gly Ala Gly Gly Ala Gly Gly Ala Gly Thr Thr Thr Gly Thr Gly Thr
 785 790 795 800
 Gly Cys Gly Ala Gly Cys Cys Gly Cys Cys Thr Cys Thr Cys Ala Thr
 805 810 815
 Cys Ala Cys Cys Cys Ala Gly Cys Ala Cys Ala Cys Ala Cys
 820 825 830
 Ala Ala Gly Thr Thr Gly Cys Thr Gly Gly Thr Thr Cys Thr Gly Gly
 835 840 845
 Ala Gly Gly Gly Cys Cys Ala Gly Gly Cys Gly Gly Cys Cys Ala Cys
 850 855 860
 Ala Cys Thr Cys Ala Ala Gly Thr Gly Cys Ala Ala Ala Gly Cys Cys
 865 870 875 880

Ala Thr Thr Gly Gly Gly Gly Ala Cys Cys Cys Cys Ala Gly Cys Cys
 885 890 895

Cys Cys Cys Thr Thr Ala Thr Cys Cys Ala Cys Thr Gly Gly Gly Thr
 900 905 910

Ala Gly Cys Cys Cys Cys Cys Gly Ala Thr Gly Ala Cys Cys Gly Cys
 915 920 925

Cys Thr Gly Gly Thr Ala Gly Gly Gly Ala Ala Cys Thr Cys Cys Thr
 930 935 940

Cys Ala Ala Gly Gly Ala Cys Cys Gly Cys Thr Gly Thr Cys Thr Ala
 945 950 955 960

Thr Gly Ala Cys Ala Ala Thr Gly Gly Cys Ala Cys Cys Cys Thr Gly
 965 970 975

Gly Ala Cys Ala Thr Cys Thr Thr Cys Ala Thr Cys Ala Cys Cys Ala
 980 985 990

Cys Ala Thr Cys Thr Cys Ala Gly Gly Ala Cys Ala Gly Thr Gly Gly
 995 1000 1005

Thr Gly Cys Cys Thr Thr Cys Ala Cys Cys Thr Gly Cys Ala Thr Thr
 1010 1015 1020

Gly Cys Thr Gly Cys Cys Ala Ala Thr Gly Cys Thr Gly Cys Cys Gly
 1025 1030 1035 1040

Gly Ala Gly Ala Gly Gly Cys Cys Ala Cys Gly Gly Cys Cys Ala Thr
 1045 1050 1055

Gly Gly Thr Gly Gly Ala Gly Gly Thr Cys Thr Cys Cys Ala Thr Cys
 1060 1065 1070

Gly Thr Cys Cys Ala Gly Cys Thr Gly Cys Cys Ala Cys Ala Cys Cys
 1075 1080 1085

Thr Cys Ala Gly Cys Ala Ala Cys Ala Gly Cys Ala Cys Cys Ala Gly
 1090 1095 1100

Cys Cys Gly Cys Ala Cys Thr Gly Cys Ala Cys Cys Cys Cys Cys Cys
 1105 1110 1115 1120

Ala Ala Gly Thr Cys Cys Cys Gly Cys Cys Thr Cys Thr Cys Ala Gly
 1125 1130 1135

Ala Cys Ala Thr Cys Ala Cys Thr Gly Gly Cys Thr Cys Cys Ala Gly	1140	1145	1150
Cys Ala Ala Gly Ala Cys Cys Ala Gly Cys Cys Gly Gly Gly Gly Ala	1155	1160	1165
Gly Gly Thr Gly Gly Ala Gly Gly Cys Ala Gly Thr Gly Gly Gly Gly	1170	1175	1180
Gly Cys Gly Gly Ala Gly Ala Gly Cys Cys Thr Cys Cys Cys Ala Ala	1185	1190	1195
Ala Ala Gly Cys Cys Cys Cys Cys Cys Gly Gly Ala Ala Cys Gly Gly	1205	1210	1215
Gly Cys Thr Gly Thr Gly Cys Thr Thr Gly Thr Gly Thr Cys Thr Gly	1220	1225	1230
Ala Ala Gly Thr Gly Ala Cys Cys Ala Cys Cys Ala Cys Cys Thr Cys	1235	1240	1245
Gly Gly Cys Cys Cys Thr Gly Gly Thr Cys Ala Ala Gly Thr Gly Gly	1250	1255	1260
Thr Cys Thr Gly Thr Cys Ala Gly Cys Ala Ala Gly Thr Cys Ala Gly	1265	1270	1275
Cys Ala Cys Cys Cys Cys Gly Gly Gly Thr Gly Ala Ala Gly Ala Thr	1285	1290	1295
Gly Thr Ala Cys Cys Ala Gly Cys Thr Gly Cys Ala Gly Thr Ala Cys	1300	1305	1310
Ala Ala Cys Thr Gly Cys Thr Cys Thr Gly Ala Cys Gly Ala Thr Gly	1315	1320	1325
Ala Gly Gly Thr Ala Cys Thr Gly Ala Thr Thr Thr Ala Cys Ala Gly	1330	1335	1340
Gly Ala Thr Gly Ala Thr Cys Cys Cys Ala Gly Cys Cys Thr Cys Cys	1345	1350	1355
Ala Ala Cys Ala Ala Gly Gly Cys Cys Thr Thr Cys Gly Thr Gly Gly	1365	1370	1375
Thr Cys Ala Ala Cys Ala Ala Cys Cys Thr Gly Gly Thr Gly Thr Cys	1380	1385	1390

Ala Gly Gly Gly Ala Cys Thr Gly Gly Cys Thr Ala Cys Gly Ala Cys
1395 1400 1405

Thr Thr Gly Thr Gly Thr Gly Thr Gly Cys Thr Gly Gly Cys Cys Ala
1410 1415 1420

Thr Gly Thr Gly Gly Gly Ala Thr Gly Ala Cys Ala Cys Ala Gly Cys
1425 1430 1435 1440

Cys Ala Cys Gly Ala Cys Ala Cys Thr Cys Ala Cys Gly Gly Cys Cys
1445 1450 1455

Ala Cys Cys Ala Ala Cys Ala Thr Cys Gly Thr Gly Gly Gly Cys Thr
1460 1465 1470

Gly Cys Gly Cys Cys Cys Ala Gly Thr Thr Cys Thr Thr Cys Ala Cys
1475 1480 1485

Cys Ala Ala Gly Gly Cys Thr Gly Ala Cys Thr Ala Cys Cys Cys Gly
1490 1495 1500

Cys Ala Gly Thr Gly Cys Cys Ala Gly Thr Cys Cys Ala Thr Gly Cys
1505 1510 1515 1520

Ala Cys Ala Gly Cys Cys Ala Gly Ala Thr Thr Cys Thr Gly Gly Gly
1525 1530 1535

Cys Gly Gly Cys Ala Cys Cys Ala Thr Gly Ala Thr Cys Cys Thr Gly
1540 1545 1550

Gly Thr Cys Ala Thr Cys Gly Gly Gly Gly Cys Ala Thr Cys Ala
1555 1560 1565

Thr Cys Gly Thr Gly Gly Cys Cys Ala Cys Gly Cys Thr Gly Cys Thr
1570 1575 1580

Gly Gly Thr Cys Thr Thr Cys Ala Thr Cys Gly Thr Cys Ala Thr Cys
1585 1590 1595 1600

Cys Thr Cys Ala Thr Gly Gly Thr Gly Cys Gly Cys Thr Ala Cys Ala
1605 1610 1615

Ala Gly Gly Thr Cys Thr Gly Cys Ala Ala Cys Cys Ala Cys Gly Ala
1620 1625 1630

Gly Gly Cys Cys Cys Cys Cys Ala Gly Cys Ala Ala Gly Ala Thr Gly
1635 1640 1645

Gly Cys Ala Gly Cys Gly Gly Cys Cys Gly Thr Gly Ala Gly Cys Ala
 1650 1655 1660

Ala Thr Gly Thr Gly Thr Ala Cys Thr Cys Gly Cys Ala Gly Ala Cys
 1665 1670 1675 1680

Cys Ala Ala Cys Gly Gly Cys Gly Cys Cys Cys Ala Gly Cys Cys Ala
 1685 1690 1695

Cys Cys Gly Cys Cys Thr Cys Cys Ala Ala Gly Cys Ala Gly Cys Gly
 1700 1705 1710

Cys Ala Cys Cys Ala Gly Cys Cys Gly Gly Gly Gly Cys Cys Cys Cys
 1715 1720 1725

Gly Cys Cys Gly Cys Ala Gly Gly Gly Cys Cys Cys Gly Cys Cys Gly
 1730 1735 1740

Ala Ala Gly Gly Thr Gly Gly Thr
 1745 1750

<210> 21
 <211> 581
 <212> PRT
 <213> Homo sapiens

<400> 21
 Ala Val Val Asp Ala Cys Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser
 1 5 10 15

Glu Ser Leu Gly Thr Leu Cys Pro Ser Lys Gly Leu Leu Phe Val Pro
 20 25 30

Pro Asp Ile Asp Arg Arg Thr Val Glu Leu Arg Leu Gly Gly Asn Phe
 35 40 45

Ile Ile His Ile Ser Arg Gln Asp Phe Ala Asn Met Thr Gly Leu Val
 50 55 60

Asp Leu Thr Leu Ser Arg Asn Thr Ile Ser His Ile Gln Pro Phe Ser
 65 70 75 80

Phe Leu Asp Leu Glu Ser Leu Arg Ser Leu His Leu Asp Ser Asn Arg
 85 90 95

Leu Pro Ser Leu Gly Glu Asp Thr Leu Arg Gly Leu Val Asn Leu Gln
 100 105 110

His Leu Ile Val Asn Asn Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala
 115 120 125

Phe Glu Asp Phe Leu Leu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn
 130 135 140

Asn Leu His Gly Leu Pro Trp Asp Ser Val Arg Arg Met Val Asn Leu
 145 150 155 160

His Gln Leu Ser Leu Asp His Asn Leu Leu Asp His Ile Ala Glu Gly
 165 170 175

Thr Phe Ala Asp Leu Gln Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn
 180 185 190

Arg Leu Gln Lys Leu Pro Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala
 195 200 205

Ser Ala Leu Thr Ala Thr Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe
 210 215 220

Gly Gly Asn Pro Leu His Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg
 225 230 235 240

Leu Glu Arg Asp Asp Asp Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu
 245 250 255

Lys Gly Arg Tyr Phe Trp His Val Arg Glu Glu Glu Phe Val Cys Glu
 260 265 270

Pro Pro Leu Ile Thr Gln His Thr His Lys Leu Leu Val Leu Glu Gly
 275 280 285

Gln Ala Ala Thr Leu Lys Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu
 290 295 300

Ile His Trp Val Ala Pro Asp Asp Arg Leu Val Gly Asn Ser Ser Arg
 305 310 315 320

Thr Ala Val Tyr Asp Asn Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser
 325 330 335

Gln Asp Ser Gly Ala Phe Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu
 340 345 350

Ala Thr Ala Met Val Glu Val Ser Ile Val Gln Leu Pro His Leu Ser
 355 360 365

Asn Ser Thr Ser Arg Thr Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile
 370 375 380

Thr Gly Ser Ser Lys Thr Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly
 385 390 395 400

Glu Pro Pro Lys Ser Pro Pro Glu Arg Ala Val Leu Val Ser Glu Val
 405 410 415

Thr Thr Thr Ser Ala Leu Val Lys Trp Ser Val Ser Lys Ser Ala Pro
 420 425 430

Arg Val Lys Met Tyr Gln Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val
 435 440 445

Leu Ile Tyr Arg Met Ile Pro Ala Ser Asn Lys Ala Phe Val Val Asn
 450 455 460

Asn Leu Val Ser Gly Thr Gly Tyr Asp Leu Cys Val Leu Ala Met Trp
 465 470 475 480

Asp Asp Thr Ala Thr Thr Leu Thr Ala Thr Asn Ile Val Gly Cys Ala
 485 490 495

Gln Phe Phe Thr Lys Ala Asp Tyr Pro Gln Cys Gln Ser Met His Ser
 500 505 510

Gln Ile Leu Gly Gly Thr Met Ile Leu Val Ile Gly Gly Ile Ile Val
 515 520 525

Ala Thr Leu Leu Val Phe Ile Val Ile Leu Met Val Arg Tyr Lys Val
 530 535 540

Cys Asn His Glu Ala Pro Ser Lys Met Ala Ala Ala Val Ser Asn Val
 545 550 555 560

Tyr Ser Gln Thr Asn Gly Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro
 565 570 575

Ala Gly Ala Pro Pro
 580

<210> 22

<211> 788

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: KIAA_predicted

<400> 22

Met Glu Thr Leu Leu Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala
1 5 10 15

Val Val Asp Ala Cys Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu
20 25 30

Ser Leu Gly Thr Leu Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro
35 40 45

Asp Ile Asp Arg Arg Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile
50 55 60

Ile His Ile Ser Arg Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp
65 70 75 80

Leu Thr Leu Ser Arg Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe
85 90 95

Leu Asp Leu Glu Ser Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu
100 105 110

Pro Ser Leu Gly Glu Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His
115 120 125

Leu Ile Val Asn Asn Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe
130 135 140

Glu Asp Phe Leu Leu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn
145 150 155 160

Leu His Gly Leu Pro Trp Asp Ser Val Arg Arg Met Val Asn Leu His
165 170 175

Gln Leu Ser Leu Asp His Asn Leu Leu Asp His Ile Ala Glu Gly Thr
180 185 190

Phe Ala Asp Leu Gln Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg
195 200 205

Leu Gln Lys Leu Pro Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser
210 215 220

Ala Leu Thr Ala Thr Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly

225		230		235		240
Gly Asn Pro Leu His Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu						
	245		250		255	
Glu Arg Asp Asp Asp Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys						
	260		265		270	
Gly Arg Tyr Phe Trp His Val Arg Glu Glu Glu Phe Val Cys Glu Pro						
	275		280		285	
Pro Leu Ile Thr Gln His Thr His Lys Leu Leu Val Leu Glu Gly Gln						
	290		295		300	
Ala Ala Thr Leu Lys Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile						
305		310		315		320
His Trp Val Ala Pro Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr						
	325		330		335	
Ala Val Tyr Asp Asn Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln						
	340		345		350	
Asp Ser Gly Ala Phe Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala						
	355		360		365	
Thr Ala Met Val Glu Val Ser Ile Val Gln Leu Pro His Leu Ser Asn						
	370		375		380	
Ser Thr Ser Arg Thr Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr						
385		390		395		400
Gly Ser Ser Lys Thr Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Glu						
	405		410		415	
Pro Pro Lys Ser Pro Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr						
	420		425		430	
Thr Thr Ser Ala Leu Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg						
	435		440		445	
Val Lys Met Tyr Gln Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val Leu						
	450		455		460	
Ile Tyr Arg Met Ile Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn						
465		470		475		480
Leu Val Ser Gly Thr Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp						

	485		490		495
Asp Thr Ala Thr Thr Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln	500	505	510		
Phe Phe Thr Lys Ala Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln	515	520	525		
Ile Leu Gly Gly Thr Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala	530	535	540		
Thr Leu Leu Val Phe Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys	545	550	555	560	
Asn His Glu Ala Pro Ser Lys Met Ala Ala Ala Val Ser Asn Val Tyr	565	570	575		
Ser Gln Thr Asn Gly Ala Gln Pro Pro Pro Pro Ser Ser Ala Pro Ala	580	585	590		
Gly Ala Pro Pro Gln Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu	595	600	605		
Leu Asp Phe Thr Ala Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser Ser	610	615	620		
Ser Ser Leu Gly Ser Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp	625	630	635	640	
Arg Ile Pro Pro Ser Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu	645	650	655		
Met Gly Ala Phe Ala Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu	660	665	670		
Leu Leu Asp Ser Arg Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala	675	680	685		
Arg Gly His His Ser Asp Arg Glu Pro Leu Leu Gly Pro Pro Ala Ala	690	695	700		
Arg Ala Arg Ser Leu Leu Pro Leu Pro Leu Glu Gly Lys Ala Lys Arg	705	710	715	720	
Ser His Ser Phe Asp Met Gly Asp Phe Ala Ala Ala Ala Gly Gly Val	725	730	735		
Val Pro Gly Gly Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr					

740

745

750

Lys Arg Ser Leu Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser
755 760 765

Asp Leu Val Gly Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met
770 775 780

Glu Ser Thr Val
785